

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 10:03:24 ; Search time 15.5455 Seconds
(without alignments)
3931.234 Million cell updates/sec

Title: US-09-125-005-6

Perfect score: 3384

Sequence: 1 MAQSTATSPGGTTFEHLMS.....PCKARKQPIKEETFEAIH 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851.5	25.2	395	JH0631	cellular tumor ant
2	778	23.0	367	S02193	cellular tumor ant
3	760.5	22.5	386	S51648	cellular tumor ant
4	749	22.1	396	JH0633	cellular tumor ant
5	741.5	21.9	393	JC6176	tumor suppressor p
6	741	21.9	363	A29376	cellular tumor ant
7	735.5	21.7	391	S02192	cellular tumor ant
8	724.5	21.4	391	JC6193	tumor suppressor p
9	724.5	21.4	393	DNH053	cellular tumor ant
10	718.5	21.2	393	S06594	cellular tumor ant
11	711.5	21.0	390	DNM553	cellular tumor ant
12	702	20.7	381	S38824	cellular tumor ant
13	248.5	7.3	77	I46226	cellular tumor ant
14	151.5	4.5	903	T00074	hypothetical prote
15	148.5	4.4	925	T19361	hypothetical prote
16	145	4.3	864	T85335	hypothetical prote
17	145	4.3	864	T04518	hypothetical prote
18	143	4.2	1819	T32008	hypothetical prote
19	142	4.2	964	T41547	hypothetical prote
20	139.5	4.1	1221	T13283	probable transcrip
21	133	3.9	1273	S58782	SEG31 protein - ye
22	131.5	3.9	2364	A56577	microtubule-associ
23	130.5	3.9	1026	T20569	hypothetical prote
24	129	3.8	306	A24354	extensin precursor
25	128	3.8	1241	T18311	hypothetical prote
26	127.5	3.8	784	S26638	SPR-1 protein - hu
27	127	3.8	3938	T42761	Bassoon protein -
28	126	3.7	817	S51342	verprolin - yeast
29	126	3.7	1791	T02909	hypothetical prote

30 125.5 3.7 1560 2 T02885 peroxisome prolif
31 125 3.7 963 2 T40290 hypothetical prote
32 125 3.7 1081 2 T13231 dachshund protein
33 124.5 3.7 2397 1 A55535 versican precursor
34 124 3.7 650 2 T04487 hypothetical prote
35 124 3.7 1051 1 JH0051 serine/threonine-s
36 124 3.7 1099 2 A56155 tumor suppressor p
37 123.5 3.6 1618 2 S21424 nestin - human
38 123.5 3.6 3942 2 T42730 Bassoon protein -
39 123 3.6 1065 2 T13230 dachshund isoform
40 123 3.6 1638 2 A42091 transcription acti
41 123 3.6 1969 2 T38495 hypothetical prote
42 123 3.6 2440 2 S39162 transcription coac
43 123 3.6 2441 2 S39161 CREB-binding prote
44 123 3.6 2715 2 T13049 eyelid - fruit fly
45 122.5 3.6 1072 2 T13232 dachshund protein

ALIGNMENTS

RESULT 1

JH0631

cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JH0631

R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.

Gene 112, 241-245, 1992

A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.

A:Reference number: JH0631; MUID:92210006

A:Accession: JH0631

A:Molecule type: mRNA

A:Residues: 1-396 <DER>

A:CROSS-references: GB:M75145; NID:g213828; PIDN:AAA9605.1; PID:g213829

A:Experimental source: liver

C:Comment: This protein is the product of a tumor suppressor gene, p53, whose inacti

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; ph

F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 25.2%; Score 851.5; DB 1; Length 396;

Best/Local Similarity 55.6%; Pred. No. 1.3e-51;

Matches 170; Conservative 43; Mismatches 86; Indels 7; Gaps 5;

QY 93 VPHTSPYAQS-STFDTMS-PAPVIPSNTDYPGPHFEVTFQSSAKSATWYSPLLRK 150

Db 61 VSATEPAPQPSITLDTGSPPTSTVPTTSDYPGALGFQALFLOSSTAKSVCTYSPDLNK 120

QY 151 LYCOIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHVTDVVKRCPNHELGRDNEQSAP 210

Db 121 LFCOLAKTCPIQIKVSTPPPGTAIRAMPVYKKAHVTDVVKRCPNHELGRDNEQSAP 179

QY 211 ASHLIRVEGNLSQVYDVPVGTGROSVVYVPPQVGTTEFTILYNFMCNSSCVGGMNRRP 270

Db 180 RGLVLRVEGNLSQVYDVPVGTGROSVVYVPPQVGTTEFTILYNFMCNSSCVGGMNRRP 239

QY 271 ILIITLWRDQVIGRRSFEGRICACPRGRKADHDHYREQALN-ESSAKNGAASKRA 329

Db 240 ILIITLWRDQVIGRRSFEGRICACPRGRKADHDHYREQALN-ESSAKNGAASKRA 299

QY 330 FKQSPAPVAGVKKRRH---GDEDTYVQVGRGNFEILMKLESLELMELVPOPLV 386

Db 300 MKEASLPAPQPGASKTKSSPAVSDEDTYVQVGRGNFEILMKLESLELMELVPOPLV 359

QY 387 DSYRQQ 392

Db 360 DKYRQK 365

RESULT 2

S02193

246

Db 173 TEVRRCPHRS---SEGDLAPPOHLIRVEGNMAEYLDKQTRHSHVVPYEPVGV 229
 QY 247 TEFTILYNFNCSSCVGMNRRPILIIITLEMRDGOVLGRSFEGRICACGRDRKAD 306
 Db 230 SDCTIHYNWCNSCGMNRRLIITILEPSGNLLGRNSFEVRICACGRDRRVEE 289
 QY 307 DHYREQ---QALNESSAKNGAKRAFKQSPAPVAPALGAGVYKRRHGDEDEYYLYQVRG 362
 Db 290 KNFKQKGPCELPKSAKRALPNTSSPQP-----KTKTLDGEYFTLKIRQ 338
 QY 363 ENFEILMKESLEME 379
 Db 339 ERFKMFQELNEALEKD 355

RESULT 5

JC6176

tumor suppressor protein p53 - Chinese hamster

C:Species: Cricetus griseus (Chinese hamster)

C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999

C:Accession: JC6176

R:Lee, H.; Larner, J.M.; Hamlin, J.L.

Gene 184, 177-183, 1997

A:Title: Cloning and Characterization of Chinese hamster p53 cDNA.

A:Reference number: JC6176; MUID:97183659

A:Contents: liver

A:Accession: JC6176

A:Molecule type: mRNA

A:Residues: 1-393 <LEE>

A:Cross-references: GB:U50395; NID:g1842229; PIDN:AA03040.1; PID:g1842230

C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage
 ligation, and recombination by protein/protein interactions.

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: liver; tumor

Query Match 21.9%; Score 741.5; DB 2; Length 393;
 Best Local Similarity 43.7%; Pred. No. 5.7e-44;
 Matches 162; Conservative 57; Mismatches 111; Indels 41; Gaps 8;

QY 14 TPEHLWSSLEDPSTYFDLPQSSRCNNEVGGTSSMDVFLHGTYSVMAQNLSSITMD 73
 Db 18 TFSDLWKLPPNNVLSTLPSS-----DSIEELFLESNVTGNLSDSGALQGVAA 66

QY 74 QMSSRAASAPYTPHSAASVTHSPYAPQSPSTEDTSPAPVIPSNTDYPGPHFEVTFQ 133
 Db 67 AAATAEDPVTTAPVASAPA-TPWPLSS-----VPSYKTFQGDYGRGLFLH 115

QY 134 SSTAKSATWYSPLLKLYCIATCTPIQIKVSTPPPPPTAIRAMPYKAEHVTDVYKR 193
 Db 116 STAKSVCTVTSPLNLFQCLATCPVLWVNSTPPGTRVRAMAIIYKLTQMTWVR 175

QY 194 CPNHELGRDFNEGOS-APASHLIRVEGNLSQYVDDPVTGQSVVVPYPPQVGTFTTI 252
 Db 176 CPHERS---SEGDSLAPPOHLIRVEGNLHAEYLDKQTRHSHVVPYEPVGSCTTI 232

QY 253 LNFNWCNSCVGMNRRPILIIITLEMRDGOVLGRSFEGRICACGRDRKADDEHYRQ 312
 Db 233 HYNFNCNSCGMNRRLIITILEPSPGNLLGRNSFEVRICACGRDRRTEENFKK 292

QY 313 ----QALNESSAKNGAKRAFKQSPAPVAPALGAGVYKRRHGDEDEYYLYQVRGNEFEL 368
 Db 293 GEPCPELPKSAKRALPNTS--SSPP-----PKTKTLDGEYFTLKIRCHERFAMF 341

QY 369 MKLESLEME 379
 Db 342 QELNEALEKD 352

RESULT 6

A29376

cellular tumor antigen p53 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A29376; S61531; S72313; I51639
 R:Sousi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
 Oncogene 1, 71-78, 1987
 A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a prot
 A:Reference number: A29376; MUID:88143684
 A:Accession: A29376

A:Molecule type: mRNA

A:Residues: 1-363 <SOU>

A:Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962

R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knochel, W.

Oncogene 9, 109-120, 1994

A:Title: Overexpression of wild-type p53 interferes with normal development in Xenop
 A:Reference number: I51639; MUID:94134403

A:Accession: S61531

A:Molecule type: mRNA

A:Residues: 1-293, 295-363 <HOE>

A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514

R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.

submitted to the EMBL Data Library, March 1994

A:Reference number: S72313

A:Accession: S72313

A:Molecule type: mRNA

A:Residues: 1-51, 53-70, 72-293, 295-363 <HOW>

A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; ph
 F:150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.9%; Score 741; DB 1; Length 363;
 Best Local Similarity 41.7%; Pred. No. 5.5e-44;
 Matches 169; Conservative 54; Mismatches 92; Indels 90; Gaps 12;

QY 1 MAQSTATSPD---GGTTFEHLWSSLEPD-----STYFDLPQSSRCNNEVVGCT 45
 Db 1 MEPSSETGMDPPLSQSTETFEWLWLL-PDPLQTVTCRLDNLSEFPDYPLA----- 48

QY 46 DSSMDVFLHGTYSVMAQNLSSITMDQSSRAASAPYTPHSAASVTHSPYAPQSPST 105
 Db 49 -ADMTVLQ-EGLMGN-----AVPTVTSCA----- 70

QY 106 FDTMSPAPVIPSNTDYPGPHFEVTFQOSSTAKSATWYSPLLKLYCIATCTPIQIKV 165
 Db 71 -----VPSTDDYAGKYGLQDFQNGTAKSVTCTYSPELNKLFCQLAKTCLPLVRV 121

QY 166 STPPPPGTAIRAMPYKAEHVTDVYKCPNHELGRDFNEGQ-SAPASHLIRVEGNLSQ 224
 Db 122 ESPPPRGSLTATAYKKSEHVAEVYKCPHHE--RSVEPGEADAAPPSHLMRVENLQAY 179

QY 225 YVDDPVTGQSVVVPYPPQVGTFTTIYFNMCNSCVGMNRRPILIIITLEMRDGOV 284
 Db 180 XMEDVNSGRHSCVYEPGQVGTCTTVLYNMCNSCGMNRRLIITILETPQGLL 239

QY 285 LGRSFEGRICACGRDRKADDEHYRQOALNESSAKNGAKRAFKQSPAPVAPALGAGV 344
 Db 240 LGRRCFEVRVCACGRDRRTEDNYTKRGLKPS-----GKRELAHPSPSEPL---P 289

QY 345 KKRKRR---HGEDETYLYQVRGNEFELMKLESLEMELVPPQLV 386
 Db 290 KKLVLVDDDEIFLIRKGRSRVEMIKKLNDALELQESLDQKV 334

RESULT 7

S02192

cellular tumor antigen p53 - rat

N:Alternate names: gene p53 protein; nuclear oncoprotein p53

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S02192; S41149

R;Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; MUID:89083585
A:Accession: S02192

A:Molecule type: mRNA
A:Residues: 1-391 <SOU>
A:Cross-references: EMBL:X13058; NID:956828; PIDN:CAA31457.1; PID:956829
R;Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268
A:Accession: S41149

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'W', 175-391 <HUL>
A:Cross-references: EMBL:L07909
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:

A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.7%; Score 735.5; DB 1; Length 391;
Best Local Similarity 42.8%; Pred. No. 1.5e-43;
Matches 167; Conservative 55; Mismatches 87; Indels 81; Gaps 12;

QY 14 TFEHLNLSLEPDTYFDLPQSSRGNNVVGTTDSSMDVYF-----HLEGMTTSVMAQFN 66

Db 18 TFCWLKLLPPDDI-----LPTTA-----TGSPNSMEDLFPQDVAAELLEG----- 58

QY 67 LLSTMDQMSRAASPTTPEHAASVTPHSYAPQSPSTFTDMSAPV----- 114

Db 59 -----PEALQV--SAPAAQEPG--TEAPAPVAPASATPWPLSS 93

QY 115 -IPNTDYPGPHFETVTFQOSTAKSATWTSYPLKLYCQIAKTCPIQIKVSTPPPGT 173

Db 94 SVPSQKTYQNGYFHLGFLQSTAKSVMTCTYSISLNKLFQCLAKTCVQLWVSTPPGT 153

QY 174 AIRAMPYKKAHVTDVWRKPCNHELGRDFNEGOSAPASHLIRVEGNLSQYVDDPVTGR 233

Db 154 RVRAMAIYKKSQHTVEVRCPHRCSD-GDG-LAPPQHLIRVEGNFYAEYLDQRTFR 211

QY 234 QSVVYPEPQVCTETTYLNFMCNSCGVGMNRRPILITILEMDRGVGLGRSFEGR 293

Db 212 HSNVYVPEPVGSDYTTTHYKMCNSCGMGNRRPILITILEDSSGNLLGRDSFEVR 271

QY 294 ICACPGRRDKADHDHYEQO-----ALNESSAKNGAASKRAFQSPAPVAPALGAGVKRRH 349

Db 272 VCACPGRRDTEENRKEEHCPELPGSA-----KRALPTSTSSPO-----QKKP 320

QY 350 GDEITYYLVGRNFEILMKLESLEME 379

Db 321 LDGEYFTKIRGRERFEMRELNEALEKD 350

RESULT 8

JC6193

tumor suppressor p53 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000

C:Accession: JC6193

R;Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.

Gene 185, 169-173, 1997

A:Title: cDNA cloning and immunological characterization of rabbit p53.

A:Reference number: JC6193; MUID:97208669

A:Accession: JC6193

A:Molecule type: mRNA

A:Residues: 1-391 <LEA>

A:Cross-references: EMBL:X90592; NID:g1532043; PIDN:CAA62216.1; PID:g1532044

C:Genetics:

A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: tumor

Query Match 21.4%; Score 724.5; DB 2; Length 391;
Best Local Similarity 43.5%; Pred. No. 8.6e-43;
Matches 165; Conservative 54; Mismatches 103; Indels 57; Gaps 10;

QY 21 SLEP---DSYFDLPQSSRGNNVVGTTDSSMDVHLEGMTTSVMAQFNLLSSMTDQMS 77

Db 9 SLEPPLSQEFTFSLWKLLENL-----LTSLNPPVDDLLSLED----- 48

QY 78 RAASAPYTPPEHAASVP--THSYAPQSPSTFTDMSAPV-----IPSTNDYFGPHFE 128

Db 49 -VANWLNEDEEGLRYPAAPAPAPAPAPAPAPATSNPLSSVPSQRTYHGTNGFR 107

QY 129 VTQQSTAKSATWTSYPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHV 188

Db 108 LGFLHSGTAKSVCTYSPCLNKLFCOLAKTCVQLWVSTPPGTRVRAMAIYKKSQHT 167

QY 189 DVYKPCNHELGRDFNEGOSAPASHLIRVEGNLSQYVDDPVTGRQSVVYVPEPQV 248

Db 168 EVVRRCPHRCSD-SDG-LAPPQHLIRVEGNLRAEYLDQRTFRHVSVYVPEPVGSD 225

QY 249 FTTILYFMCNSCGVGMNRRPILITILEMDRGVGLGRSFEGRICACPGRRDKADE 308

Db 226 CTTIHYKMCNSCGMGNRRPILITILEDSSGNLLGRNSFEVRCACPGRRDTEEN 285

QY 309 YRQOALNESSAKNG-----AASKRAFQSPAPVAPALGAGVKRRHGEDYIYQVR 360

Db 286 FR-----KKGPCPELPGSKRAL-----PTTTDSSPQTKKPLDGEYFIKIR 331

QY 361 GRENFEILMKLESLEME 379

Db 332 GREFEMRELNEALEKD 350

RESULT 9

DNUH53

cellular tumor antigen p53 [validated] - human

N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation sup

C:Species: Homo sapiens (man)

C:Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000

C:Accession: A25224; A43073; J0436; S40773; S42669; A22837; A55060; B25397;

4903; 158354; 178850; 152081; S60153

R;Lamb, P.; Crawford, L.

Mol. Cell. Biol. 6, 1379-1385, 1986

A:Title: Characterization of the human p53 gene.

A:Reference number: A25224; MUID:87064416

A:Accession: A25224

A:Molecule type: DNA

A:Residues: 1-393 <LAMB>

A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAAS9987.1;

R;Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

Gene 70, 245-252, 1988

A:Title: A variation in the structure of the protein-coding region of the human p53

A:Reference number: J0436; MUID:89108008

A:Accession: A43073

A:Molecule type: DNA

A:Residues: 1-393 <BUCL>

A:Cross-references: EMBL:M22898; NID:g189474

A:Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro

A:Accession: J0436

A:Molecule type: DNA

A:Residues: 1-71, 'P', 73-393 <BUC2>

A:Cross-references: EMBL:M22898; NID:g189474; PIDN:AAAS9988.1; PID:g189476

R;Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.

submitted to the EMBL Data Library, August 1990.

A:Reference number: S40773

A:Accession: S40773

A:Molecule type: DNA

A:Residues: 1-393 <CHUD>

A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
 R:Matlaghewski, G.; Lamb, P.; Pin, D.; Peacock, J.; Crawford, L.; Benchimol, S.
 EMBO J. 3, 3257-3262, 1984
 A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53 protein in COS cells
 A:Reference number: S42669; MUID:85126934
 A:Accession: S42669
 A:Molecule type: mRNA
 A:Residues: 101-393 <MK1>
 A:Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PID:g642241
 R:Zakut-Houri, R.; Blenz-Tadmor, B.; Givol, D.; Oren, M.
 EMBO J. 4, 1251-1255, 1985
 A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
 A:Reference number: A22837; MUID:85230577
 A:Accession: A22837
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-393 <2AK>
 A:Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
 R:Harlow, E.; Williamson, N.M.; Ralston, R.; Hellman, D.M.; Adams, T.E.
 Mol. Cell. Biol. 5, 1601-1610, 1985
 A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53
 A:Reference number: A55060; MUID:85267676
 A:Accession: A55060
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-272, 'H', 274-393 <HAR>
 A:Cross-references: GB:X03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
 A:Experimental source: clone pR4-2, cell line A431
 R:Haris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.
 Mol. Cell. Biol. 6, 4650-4656, 1986
 A:Title: Molecular basis for heterogeneity of the human p53 protein.
 A:Reference number: A93086; MUID:87089826
 A:Accession: A25397
 A:Molecule type: mRNA
 A:Residues: 1-78, 'T', 80-393 <HAR>
 A:Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
 A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
 A:Accession: B25397
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>
 A:Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
 A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
 R:Matlaghewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
 Mol. Cell. Biol. 7, 961-963, 1987
 A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
 A:Reference number: S42452; MUID:87144273
 A:Accession: S42452
 A:Molecule type: mRNA; DNA
 A:Residues: 66-71, 'P', 73-79 <MK12>
 A:Experimental source: clone lambda C113
 A:Note: 72-Cys was also found, and appears to represent a polymorphism
 A:Accession: S42453
 A:Molecule type: mRNA; DNA
 A:Residues: 66-79 <MK13>
 A:Experimental source: clone J6K
 R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.
 EMBO J. 10, 2879-2887, 1991
 A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
 A:Reference number: I38082; MUID:92007731
 A:Accession: I38082
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-189, 'L', 190-393 <F01>
 A:Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
 A:Note: deletion of a C nucleotide causes a frameshift at position 566
 A:Accession: I38083
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-192, 'R', 194-393 <F02>
 A:Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PID:g506435
 A:Accession: I38084
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-393 <F03>
 A:Cross-references: EMBL:X60012; NID:g506436; PIDN:CAA42627.1; PID:g506437

A:Accession: I38085
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-245, 'T', 247-393 <F04>
 A:Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PID:g506439
 A:Accession: I38086
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-236, 'I', 238-393 <F05>
 A:Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441
 A:Accession: I38087
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-247, 'Q', 249-393 <F06>
 A:Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443
 A:Accession: I38088
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
 A:Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA42631.1; PID:g506445
 A:Accession: I38089
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-247, 'Q', 249-393 <F08>
 A:Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
 A:Accession: I38090
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
 A:Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506449
 A:Accession: I38091
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212, 'Q', 214-393 <F10>
 A:Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451
 A:Accession: I38092
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-253, 'D', 255-393 <F11>
 A:Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453
 A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
 R:Putreal, P.A.; Barrett, J.C.; Wiseman, R.W.
 Nucleic Acids Res. 19, 5977, 1991
 A:Title: An Alu polymorphism intragenic to the TP53 gene.
 A:Reference number: I38093; MUID:92107726
 A:Accession: I38093
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393 <FUT>
 A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
 R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakai
 Cancer Res. 51, 5800-5805, 1991
 A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell
 A:Reference number: A44905; MUID:92034678
 A:Accession: A44905
 A:Molecule type: DNA
 A:Residues: 246-247, 'W', 249-250 <YAM>
 A:Cross-references: GB:S63157; NID:g337829; PIDN:AAE20140.1; PID:g237830
 A:Note: sequence extracted from NCI backbone (NCBI:63157, NCBIP:63158)
 R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
 Oncogene 6, 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to det
 A:Reference number: I58354; MUID:91296386
 A:Accession: I58354
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-references: GB:S41969; NID:g1679931; PIDN:AAE19324.1; PID:g232814
 A:Accession: I78850
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>

A:Accession: S38823
 A:Molecule type: mRNA
 A:Residues: 1-167, 'G', 169-233, 'I', 235-390 <ARA2>
 A:Cross-references: EMBL:M13873
 R:Atai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 submitted to the EMBL Data Library, July 1988
 A:Reference number: S40014
 A:Accession: S40014
 A:Molecule type: mRNA
 A:Residues: 1-167, 'G', 169-390 <ARA3>
 A:Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39883.1; PID:g200201
 R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
 Nucleic Acids Res. 12, 5609-5626, 1984
 A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the cellular tumor antigen p53
 A:Accession: 148703
 A:Cross-references: from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>
 A:Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571
 C:Comment: This DNA-binding protein plays an essential role in the regulation of cell division
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein
 F:1-44/Domain: transcription activation #status predicted <TRA>
 F:16-26/Region: conserved region I
 F:99-289/Domain: DNA-binding core #status predicted <DBC>
 F:108-121/Region: L1 loop
 F:114-139/Region: conserved region II
 F:160-192/Region: conserved region III
 F:231-252/Region: conserved region IV
 F:233-248/Region: L3 loop
 F:267-283/Region: conserved region V
 F:313-319/Region: nuclear location signal
 F:319-357/Region: tetramer association
 F:779,12,16,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
 F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
 F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

 Query Match 21.0%; Score 711.5; DB 1; Length 390;
 Best Local Similarity 43.2%; Pred. No. 6.9e-42;
 Matches 159; Conservative 64; Mismatches 104; Indels 41; Gaps 12;

 QY 14 TFEHLWSLEPDSYFDLPQSSRGNNVGGTSSMDVHLEGMTSYMAQFNLLSSTMD 73
 DB 21 TFSGLWKLPPPE----DILSPHCHMDLLLPQD--VEEF-FEGPSEAL----- 61

 QY 74 QMSRAASAPY--TPEHAASVTHSPYAPQSPSTFTMSPAPVPSNTDYPGPHFEVTF 131
 DB 62 RVSGAPAAQDPVETPGVPAPAPA--TPW--PLSSF-----VPSQTYQNGYFHLGF 110

 QY 132 QOSSTAKSATWYSPLLKLYCQIAKTCPTQIKVSTPPPPGTAIRAMPVYKAEHVTDV 191
 DB 111 LQSGTAKSVMTYSPPLNLFCLQAKTCPVQLWVSATPPAGSRVRAAIYKKSQHTVEV 170

 QY 192 KRCNHELGRDFNEGQAPASHLIRVEGNLSQYVDDPTGQSVVVPYEPVQVTEFT 251
 DB 171 RCPHHERCSD-GDG-LAPPQHLIRVEGNLYPEYLEDROTFRHSVVPYEPPEAGSEYTT 228

 QY 252 ILYNFMNCCVCGMNRRLIITILEMRDGOVLGRSFEGRICACPGDRKADHDHYRE 311
 DB 229 IHKYMNCSCMGMRRLPILITILEDSSGNLLGRDSEVRVACPGDRKADHDHYRE 288

 QY 312 QOALNESSAKNGAASKRAFQKQSPVAPALGAGVKKRHGDEDTYYLYQVGRNFEILMKL 371
 DB 289 KEVLCPELPPGSA--KRALPTCTASAPP-----QKKKPLDGEYFTLKIRGRKRFEMFREL 341

 QY 372 KESLELME 379
 DB 342 NEALELKD 349

RESULT 12
 S38824
 cellular tumor antigen p53, minor splice form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S38824; S35478
 R:Atai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3239, 1986
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
 A:Reference number: S38822; MUID:87064640
 A:Accession: S38824
 A:Molecule type: mRNA
 A:Residues: 1-381 <ARA>
 A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
 R:Han, K.A.; Kulesz-Martin, M.F.
 Nucleic Acids Res. 20, 1979-1981, 1992
 A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different
 A:Reference number: S35478; MUID:92253421
 A:Accession: S35478
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-381 <HAB>
 A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
 C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks
 a not known
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: alternative splicing; phosphoprotein; zinc
 F:1-44/Domain: transcription activation #status predicted <TRA>
 F:16-26/Region: conserved region I
 F:99-289/Domain: DNA-binding core #status predicted <DBC>
 F:108-121/Region: L1 loop
 F:114-139/Region: conserved region II
 F:160-192/Region: conserved region III
 F:168-178/Region: conserved region IV
 F:231-252/Region: conserved region V
 F:233-248/Region: L3 loop
 F:267-283/Region: conserved region V
 F:313-319/Region: nuclear location signal
 F:319-357/Region: tetramer association
 F:779,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
 F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

 Query Match 20.7%; Score 702; DB 2; Length 381;
 Best Local Similarity 41.3%; Pred. No. 3e-41;
 Matches 164; Conservative 69; Mismatches 114; Indels 50; Gaps 14;

 QY 14 TFEHLWSLEPDSYFDLPQSSRGNNVGGTSSMDVHLEGMTSYMAQFNLLSSTMD 73
 DB 21 TFSGLWKLPPPE----DILSPHCHMDLLLPQD--VEEF-FEGPSEAL----- 61

 QY 74 QMSRAASAPY--TPEHAASVTHSPYAPQSPSTFTMSPAPVPSNTDYPGPHFEVTF 131
 DB 62 RVSGAPAAQDPVETPGVPAPAPA--TPW--PLSSF-----VPSQTYQNGYFHLGF 110

 QY 132 QOSSTAKSATWYSPLLKLYCQIAKTCPTQIKVSTPPPPGTAIRAMPVYKAEHVTDV 191
 DB 111 LQSGTAKSVMTYSPPLNLFCLQAKTCPVQLWVSATPPAGSRVRAAIYKKSQHTVEV 170

 QY 192 KRCNHELGRDFNEGQAPASHLIRVEGNLSQYVDDPTGQSVVVPYEPVQVTEFT 251
 DB 171 RCPHHERCSD-GDG-LAPPQHLIRVEGNLYPEYLEDROTFRHSVVPYEPPEAGSEYTT 228

 QY 252 ILYNFMNCCVCGMNRRLIITILEMRDGOVLGRSFEGRICACPGDRKADHDHYRE 311
 DB 229 IHKYMNCSCMGMRRLPILITILEDSSGNLLGRDSEVRVACPGDRKADHDHYRE 288

 QY 312 QOALNESSAKNGAASKRAFQKQSPVAPALGAGVKKRHGDEDTYYLYQVGRNFEILMKL 371
 DB 289 KEVLCPELPPGSA--KRALPTCTASAPP-----QKKKPLDGEYFTLKIRGRKRFEMFREL 341

QY 372 KESLELMELVQPLVDVSYRQOQLLRP-SHLQPPSY 407
Db 342 NEALELK-----DAHATEESGDSRAHSSLLQPRAF 370

RESULT 13

cellular tumor antigen p53 - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
C:Accession: I46226

R:Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.
Anticancer Res. 14, 2039-2046, 1994
A:Title: The canine p53 gene is subject to somatic mutations in thypoid carcinoma.
A:Reference number: I46226; MUID:59150524
A:Accession: I46226

A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-77 <DEV>
A:Cross-references: GB:L27630; NID:q508454; PIDN:AAC37327.1; PID:q508455
C:Genetics:
A:Gene: p53
A:Introns: 24/1; 51/3
C:Superfamily: cellular tumor antigen p53

Query Match 7.3%; Score 248.5; DB 2; Length 77;
Best Local Similarity 61.5%; Pred. No. 1.1e-10;
Matches 48; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

QY 183 KAEHTVDVKKCPNHELRGNFGQSQAPASHLIRVEGNLSQYDDPVTGRQSVVVPYEP 242
Db 1 KSEFTEVVRCPHRCSDSDG-LAPPHLIRVEGNLRKYLDDYTFRRHSVVVPYEP 59

QY 243 PQVGTEFTILYNFMCS 260
Db 60 PEVGFDYTHYNTMCS 77

RESULT 14

T00074
hypotheical protein KIAA0460 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C:Accession: T00074

R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4, 345-349, 1997
A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
A:Reference number: Z14085; MUID:98116662
A:Accession: T00074
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-903 <SEK>
A:Cross-references: EMBL:AB007929; NID:q3413881; PIDN:BA32305.1; PID:q3413882
A:Experimental source: Brain
C:Genetics:
A:Note: KIAA0460

Query Match 4.5%; Score 151.5; DB 2; Length 903;
Best Local Similarity 21.1%; Pred. No. 0.018;
Matches 175; Conservative 75; Mismatches 253; Indels 327; Gaps 45;

QY 3 QSTATSPD-----GGTTEHL-----WSSLEPSTYFDLPQSSRGNNVVGTD 46
Db 102 ESESTSPSLEMKIHNFLKGNPGFSGNLNIPILSLGSSA-----PSESHPSDFQRGPTS 156

QY 47 SSMDFVLEGM-----TTSVMAQFNLLSSTWDQMSSRAASA-SP-- 84
Db 157 TSID-NIDGTPVDRSGTPTQDEMMDKPTSSVDVTSLLSKIIISGSSPSTSTREPPP 214

QY 85 -----YTPHAASVPTH-----SPYAPQSPSTFDTMSPAPVPSNT----- 119
Db 215 GRDESYPRELNSVSTRPFRGLASESPYKQPSDGM-E-RPSSLMDSSQEKYPTDSTFQED 272

QY 120 -----DYPGPHFEVTFQOOSTAKSA-----TWYSPLLKKLYCOIAKTCPIQIKV 165
Db 273 EDYRDEYSGPPSPSAMNLEKKKILKSSKLSDDTEYQPISS-YSHRAQ--EFGYKS 329
QY 166 STPPPGTATAMPYKKAHVTDVVKRP-----NHELGRD-----FN 204
Db 330 AFPP-----SVRAL-----LDSSENCRLSSSPGLFGAFSVRGNPEGSDRSPSKN 376
QY 205 EGQAPASHLIRVGNLS-----QYVDDP-----VTGRQSVVVPY-BPP 243
Db 377 DSFTPDPSN-----HNSLSQSTTGHLSPQKQYDPSHPVPHRSLFSPQNTLAATGTHPP 431
QY 244 QVGEFTILYNFMCSVCGMN-----RRPILLIILEMRDQVGLRRSFEGRIC-- 295
Db 432 TSGVE--KVLASTITSTIEFNMLKNASRK-----SDDKHFGQAPSKGTPSDG 480
QY 296 -----ACPGDRKADHDHYREQQA-----LNESSAKNGA-----ASKRAF 330
Db 481 VLSNLTQPSLTATDQOQOQEEHYRIETRVSSCLDLPDSTEKGAPIETLGVHSASNRM 540
QY 331 KQSP-----PAPALGAGYKRRGDEDT-----YLLQVGRNFEFILMKLESLEL----- 377
Db 541 SGEPIQTVESIRVPGK--NRGHGREASRVGWFDLSTSGSSFDNGPSSASELASLGSGGS 598
QY 378 -----MELVP--QPLVDVSYRQOQLLRP-SHLQ-----PSYGP 409
Db 599 GGLTGFTAPYKERAPQFQESVGSFRSNFSTFEHLPPSPLEHCTPFQREPVGSSAP 658
QY 410 VLSPNKVVGM-----NKLPSV-----QLVGQPPPHSSAANTNLGPVGP 451
Db 659 PVPP--KDHGIFGRDAPTHLPSVDLSNPFTEAALAHAAAPPPPGEGHSGIPFTPPPP- 715
QY 452 MLNHHGAVPANGEMSSSHSAQSMVSGSHCTPPPYHADPSLVSF-----LTGLGCPNCIE 507
Db 716 -----PPGHESS--SGSGVPFSTPPPPPPVHDHSGVVPVPPAPLAHGVAGAYA 764
QY 508 YFTSGQLOSIYH---LQNLTIEDLGALKIPEQYRMTWRGLQDLKQGHYDYSTAQQLRSS 564
Db 765 VFPKD-----HSSLQGLTAEHFGVLPGP-----RDHGGFTQ--RDL 799
QY 565 NAATISISGGSELQQRVMEAVHFRVHTITPN-----RGGPGGG 605
Db 800 NPGLS-----RVRESLTLPSSHLEHLPHPHGGGGGG 831

RESULT 15

T19361
hypotheical protein C17G1.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T19361
R:White, S.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19114
A:Accession: T19361
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-925 <WIL>
A:Cross-references: EMBL:Z78415; PIDN:CAB01670.1; GSPDB:GN00028; CESP:C17G1.4
C:Experimental source: clone C17G1
C:Genetics:
A:Gene: CESP:C17G1.4
A:Map position: X
A:Introns: 40/3; 98/2; 295/1; 443/3; 590/3; 619/3; 691/1; 810/1; 868/3
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homol-

Query Match 4.4%; Score 148.5; DB 2; Length 925;
Best Local Similarity 21.6%; Pred. No. 0.03;
Matches 135; Conservative 74; Mismatches 232; Indels 185; Gaps 32;

QY 4 STATSPDG-GTT-----FEHLWSLEPDSYFDLPQ-----SSRGNNV 42
Db 369 STPGTSGHGTGVSNAFLSHQKPSQOQSMHNLPHHQYNONNLLSPNHGASSLSQKQH 428

Qy	43	GTDSMDVPHLGWTTSVMAQFNNLLSTMDQMSRAASPYTPEHAASVPTHSPYAP	102
Db	429	GSSPMGSSLPLANGQPSM-----TQNNQSPASTSMEPTFKEPAPVI-RHSPQMP	478
Qy	103	SSTEDTMSAP-----VIPNTDYPGPHFEVTFQ--SSTAKSATWTSPLLKLY	152
Db	479	THLASPVHPSPNGAPAYNAPSSSTKTPD-----TOORPHSPFTAVPTLPAATAAQAF	533
Qy	153	C-QIA-----STCPIQIK---YSTPPPGCTAIRAMPYKKAHV---DVVAKRCPNHEIG	200
Db	534	SANQISTKPKTSPQKKKHEDGVPEPTADTFETTVHYELPAAMFLRDLHVGPNDKVH	593
Qy	201	RDNEGOSAPASHLIRVEGNLSQYVDVPTGRQSVVPY-----PBP-----Q	244
Db	594	P-----QVEKHYSFR-----KROOLRVYPEGINSHTTPTPEPTNPTGFM	632
Qy	245	VTETFTILXNFCNCSVCGMNRAPILITITLMDRGQVLGRSFEGRICACPRDRKA	304
Db	633	QGNYPFDEKYNRVVPSQTSHG-----PPLLSRSQSHTPMI--SPNFTNASQPSISGR	682
Qy	305	DEDHYEQOALNESSAKNGAASKRAFKOSPAPVAFALGAGYKRRHGD-----DTYLVQVR	360
Db	683	-----QPAKKARSAD--ASEPFP--NVPHPPSSRGSDMRQLQOQOQLOMQOYHQHQ	731
Qy	361	GRENFETILMKLSLELM-----ELVPOPLVDYVROOQQLLRPSHLAPPSTG	408
Db	732	MOKWQOQOAAAQOQMSRMGGSPSAGPGGSQLPSLSAPLSQRADSMPLQPSQOQPMGG	791
Qy	409	PVLSPMNKVVHGKNKL-----PSVNOI-----VGQPPHSSAATPMIGPVGP-GWL	453
Db	792	PANHM-----GGQOPMNGTPTGPTVNNIGLNSNNAAGLPP-----JLSRQGDGSG	840
Qy	454	NNHGHAVPANGEMSSHSQAQSVYSGSHCTPPP-----PYHAD-----PSLV	494
Db	841	NNDFPGIPST---SSSNOAHALCAGCHHFIWPGSSTLSCLYHDCKNVYHRECTRISPSA	897
Qy	495	SFLTGLG-----CPNCIEYFTSGOLQ	515
Db	898	QMEGTQVWRVWCPSCSOFQRMQIQ	923

Search completed: November 7, 2002, 10:14:36
Job time : 20.6566 secs